REMARKS

INTRODUCTION:

In accordance with the foregoing, claims 16, 23 and 24 have been amended. No new matter is being presented, and approval and entry are respectfully requested.

Claims 16, 17, 23, 24, and 25 are under consideration. Claim 26 is withdrawn. Reconsideration is respectfully requested.

ENTRY OF RESPONSE UNDER 37 C.F.R. §1.116:

Applicants request entry of this Rule 116 Response and Request for Reconsideration because:

(a) it is believed that the amendments of claims 16, 23 and 24 put this application into condition for allowance;

(b) the amendments were not earlier presented because the Applicants believed in good faith that the cited prior art did not disclose the present invention as previously claimed;

(c) the amendments of claims 16, 23 and 24 should not entail any further search by the Examiner since no new features are being added or no new issues are being raised; and/or

(d) the amendments do not significantly alter the scope of the claims and place the application at least into a better form for appeal. No new features or new issues are being raised.

The Manual of Patent Examining Procedures sets forth in §714.12 that "[a]ny amendment that would place the case either in condition for allowance <u>or in better form for appeal</u> may be entered." (Underlining added for emphasis) Moreover, §714.13 sets forth that "[t]he Proposed Amendment should be given sufficient consideration to determine whether the claims are in condition for allowance and/or whether the issues on appeal are simplified." The Manual of Patent Examining Procedures further articulates that the reason for any non-entry should be explained expressly in the Advisory Action.

REJECTION UNDER 35 U.S.C. §112:

In the Office Action, at pages 2-8, claims 16, 17, and 23-25 were rejected under 35 U.S.C. §112, second paragraph, for the reasons set forth therein. This rejection is traversed and reconsideration is requested.

Page 4, line 27 through line 23, page 5 of the specification recite:

When the researcher searches the similar three-dimensional, structure, <u>an r.m.s.d. (root</u>

mean square distance) value is used as a scale of the similarity of the three-dimensional structures of the substances. The r.m.s.d. value is a value expressing a square root of a mean square distance between the corresponding elements constituting the substances. Empirically, the substances are thought to be exceedingly similar to each other in the case where the r.m.s.d. value between the substances is not greater than 1 Å. (emphasis added)

For instance, it is assumed that there are substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, ..., m) and b_j (i=1, 2, ..., n) are vectors expressing positions of the respective elements in the three-dimensional space. The elements constituting these substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between the corresponding elements is minimized. For example, if a_k is related to b_k (k=1, 2, ..., n), the r.m.s.d. value is obtained in the following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights:

$$r.m.s.d. = \frac{\left(\sum_{k=1}^{n} \left(w_k (Ub_k - a_k)^2\right)\right)^{\frac{1}{2}}}{n}$$

$$......(1)$$

(emphasis added).

For clarity, the definition of the r.m.s.d. value has been added to independent claims 16, 23, and 24 in accordance with page 4, line 27 through line 23, page 5 of the specification.

In addition, the wording of independent claims 16, 23 and 24 has been amended to clarify the source of the subsets (target and probe) and to eliminate redundancy. Antecedent basis has also been corrected. For clarity, the terminology "second structure

The terminologies "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence" and "wherein the tree structures are generated by successively giving correspondence to an element constituting the sets" have been added to each of the independent claims 16, 23 and 24 to show more clearly that the point sets are expressed by three-dimensional coordinates (see page 53, lines 22-24 of the specification) wherein possible correspondence is described by a tree structure created by successively giving correspondence to the element constituting the sets (see page 54, lines 13-24 of the specification).

The terminology "attribute" is given its ordinary dictionary definition. For example, in Merriam-Webster Online, attribute is defined as "1: an inherent characteristic; also, an accidental quality 2: an object closely associated with or belonging to a specific person, thing or office ... 3: a word ascribing a quality..." Examples are set forth on page 37, lines 1-10 of the specification.

The information encompassed by either a first point set or a second point set is a set of three-dimensional coordinates, and the coordinates are analyzed to determine correspondence (see above). Thus, it is respectfully submitted that the terminology "attribute" and the information encompassed by the first point set and the second point set are clear and definite.

The Examiner submits that the claim fails to delineate any positive steps that result in generating a correspondence. Amended independent claim 16 recites:

> determining whether a correspondence is present between the first point set and the second point set by, for each subset of the plurality of target subsets of secondary structures of the target structure:
> generating a first tree structure for the first point set and a second tree structure for the second point set wherein the tree structures are generated by successively giving correspondence to an element constituting the sets;
> pruning the second tree structure for the second point set in accordance with a predetermined pruning procedure; and
> determining whether the first point set and the second point set have a same attribute, and if the first point set and the second point set have the same attribute, generating a correspondence between the first point set and the second point; and
> calculating a root mean square distance (RMSD) value between elements corresponding in the first point set and the second point set to automatically determine a value for a distance between the elements of the first point set and the elements of the second point set, wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights:

$$r.m.s.d. = \frac{\left(\sum_{k=1}^{n} \left(W_k (Ub_k - a_k)^2 \right) \right)^{\frac{1}{2}}}{n}$$

......(1);

> determining whether the RMSD is less than or equal to a predetermined threshold value, and where the RMSD is less than or equal to a predetermined threshold value, generating an optimum correspondence between the first point set of and the second point set;
> determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having the optimum correspondence to the input amino acid sequence; and
> displaying by a display unit, the longest common subsequence (LCS) between the character sequence expressing the input amino acid sequence and the character sequence expressing the amino acid sequence having the optimum correspondence to the input amino acid sequence.
> (emphasis added)

It is respectfully submitted that amended independent claim 16, and similarly, amended independent claims 23 and 24, recite positive steps that result in generating a correspondence (generating a first tree structure for the first point set and a second tree structure for the second point set wherein the tree structures are generated by successively giving correspondence to an element constituting the sets; pruning the second tree structure for the second point set in accordance with a predetermined pruning procedure; and determining whether the first point set and the second point set have a same attribute, and if the first point set and the second point set have the same attribute, generating a correspondence between the first point set and the second point set). As noted above, the terminologies "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence" and "wherein the tree structures are generated by successively giving correspondence to an element constituting the sets" have been added to each of the independent claims 16, 23 and 24 to show more clearly that the point sets are expressed by three-dimensional coordinates (see page 53, lines 22-24 of the specification), wherein possible correspondence is described by a tree structure created by successively giving correspondence to the element constituting the sets (see page 54, lines 13-24 of the specification). For example, pruning is illustrated in FIG. 18, and is described on page 33, line 10 through page 37, line 25 of the specification. It is respectfully submitted that the process of "pruning" the trees is known to those skilled in the art. Hence, it is respectfully submitted that it is clear how the steps are drawn to generating and pruning a first and a second tree structure and how such is related to generating correspondences between a first and a second point set.

The amendment to include, in independent claims 16, 23 and 24, the terminology "wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i ($i=1, 2, \ldots, m$) and b_j ($i=1, 2, \ldots, n$) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights:

$$r.m.s.d. = \frac{\left(\sum_{k=1}^{n}\left(w_k(Ub_k - a_k)^2\right)\right)^{\frac{1}{2}}}{n}$$

........(1);

is submitted to explain the scope of an "element" and the terminology "point set" is described further above. Hence, it is submitted that the information being relied upon in performing an RBSD calculation is clear. For clarity, the terminology has been amended to recite "calculating a root mean square distance (RMSD) value between elements."

Independent claims 16, 23 and 24 have been amended to recite "predetermined threshold value set by a user." Thus, it is respectfully submitted that the terminology "predetermined threshold value" is now clear and definite.

It is respectfully submitted that on page 16, line 31 through page 17, line 5, the specification recites:

> The LCS detection unit 30 determines an LCS (Longest Common Subsequence), the length of LCS, and an occurrence position of the LCS between a character sequence expressing an amino acid sequence input from the input device 40 and a character sequence expressing an amino acid sequence taken from the amino acid sequence data base 50 or motif data base 60. The LCS is the longest subsequence among those which commonly occur continuously or intermittently in both character sequences, and the longest common character number is the number of characters constituting the LCS. (emphasis added)

Hence, independent claim 16 has been amended to recite: "determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence taken from an amino acid sequence data base or a motif data base having the optimum correspondence to the input amino acid sequence." Independent claims 23 and 24 have been amended similarly. Thus, the terminology "a character sequence expressing" is now submitted to be clear.

Hence, amended independent claims 16, 23 and 24 are now submitted to be definite under 35 U.S.C. §112, second paragraph, and to particularly point out and distinctly claim the subject matter which applicants regard as the invention. Since claims 17 and 25 depend from amended independent claims 16 and 24, respectively, claims 17 and 25 are definite under 35 U.S.C. §112, second paragraph, and particularly point out and distinctly claim the subject matter which applicants regard as the invention for at least the reasons amended independent claims 16 and 24 are definite under 35 U.S.C. §112, second paragraph, and particularly point out and distinctly claim the subject matter which applicants regard as the invention.

DOUBLE PATENTING:

In the Office Action, at pages 8-10, claims 16, 17, and 23 were provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claim 13 of copending Application No. 09/910,071. This rejection is traversed and reconsideration is requested.

Since U.S. Patent Application No. 09/910,071 has not yet been issued as a patent, and since the all of the claims of the instant application have not yet been indicated as allowable except for the provisional rejection, it is believed that any submission of a Terminal Disclaimer or arguments as to the non-obvious nature of the claims would be premature. MPEP 804(I)(B). As such, it is respectfully requested that the applicants be allowed to address any obviousness-type double patenting issues remaining once the rejection of the claims under 35 U.S.C. § 112 is resolved or on allowance of U.S. Patent Application No. 09/910,071.

EXAMINER'S RESPONSE TO ARGUMENTS:

In the Office Action, at pages 10-18, the Examiner responded to Applicants' arguments filed 9/11/2006.

The Examiner submitted that the terminology "R.M.S.D." is still unclear. Independent claims 16, 23 and 24 have been amended to include the definition of R.M.S.D., and for clarity, the terminology "root mean square distance (RMSD)" has been amended to recite "root mean square distance (RMSD) value." Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear. Hence, the terminology R.M.S.D. is now submitted to be clear.

The Examiner is concerned with the terminology "a first probe structure expressed by the three-dimensional coordinates of elements belonging to a first probe subset of a plurality of subsets of a secondary structure of probe structures, the first subset comprising a first point set of an amino acid sequence or a motif database." Independent claims 16, 23 and 24 have been amended to clarify the subset terminology by referring to the subsets of the target as the target subsets and the subsets of the probe as the probe subsets. Also, independent claims 16, 23 and 24 have been amended to recite "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence." Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.   Hence, the terminology cited above is now submitted to be clear.

The Examiner is concerned with the language "a target structure expressed by three-dimensional coordinates of elements belonging to a second subset of a plurality of subsets of secondary structures of the target structure, the second subset comprising a second point set of an input amino acid sequence of the target structure." Independent claims 16, 23 and 24 have been amended to clarify the "subset" language" and to recite "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence." Independent claims 16, 23 and 24

have been further amended to include the terminology "wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, \ldots, m) and b_j (i=1, 2, \ldots, n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights." Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear. Hence, said language is now submitted to be clear.

The Examiner is concerned with the terminology "dividing the second target structure into a plurality of second subsets based on secondary structures of the three-dimensional coordinates of the target structure." The "subset" language has been amended for clarity. It is respectfully submitted that the amendment to add, to independent claims 16, 23, and 24, the terminology "wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, \ldots, m) and b_j (i=1, 2, \ldots, n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights" clarifies how the division of the target structure into a plurality of subsets results in generation of a distinct set of subset structures. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with a step drawn to determining whether a correspondence is present between the first point set and the second point set by (i) generating a first tree structure for the first point set and a second tree structure for the second point set, (ii) pruning the second tree structure for the second point set, (iii) determining whether the first point set and the second point set have a same attribute, and (iv) if the first point set and the second point set have a same attribute, generating a correspondence between the first point set and the second point set. Claims 16, 23 and 24 have been amended to clarify the operations of the present invention (see above). The terminology "attribute" has its common dictionary definition, and thus is submitted to be clear. The scope of the terminology "attribute" is clear from the specification (see above). Thus, amended independent claims 16, 23 and 24 are submitted to be clear with respect to the above-cited Examiner's concern. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with the terminology "calculating a root mean square

distance (RMSD) between elements corresponding in the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure to automatically determine a distance between the elements of the first point set and the elements of the second point set." This terminology has been amended for clarity (see above). For example, the terminology "root mean square distance (RMSD)" has been amended to recite "root mean square distance (RMSD) value" and "to automatically determine a distance" has been amended to recite "to automatically determine a value for a distance." The point sets have been described by adding the terminology "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence." The "element" terminology has been clarified by adding the terminology "wherein substances expressed by a point set A={a_1, a_2, . . . , a_i, . . . , a_m} of a target subset, and a point set B={b_1, b_2, . . . , b_j, . . . , b_n} of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other." Hence, said terminology is now believed to be clear in amended independent claims 16, 23 and 24. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with the terminology "a predetermined threshold value." Said terminology has been amended to recite "a predetermined threshold value set by a user," and is now submitted to be clear in amended independent claims 16, 23 and 24. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with the terminology "a character sequence expressing the input amino acid sequence" and "a character sequence expressing the amino acid sequence." In independent claims 16, 23 and 24, said terminology has been amended for clarity to recite: "determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence taken from an amino acid sequence data base or a motif data base having the optimum correspondence to the input amino acid sequence" based on page 16, line 31 through page 17, line 2 of the specification. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

Hence, it is respectfully submitted that the Examiner's concerns have been overcome by the present amendments.

CONCLUSION:

In accordance with the foregoing, it is respectfully submitted that all outstanding objections and rejections have been overcome and/or rendered moot, and further, that all

pending claims patentably distinguish over the prior art. Thus, there being no further outstanding objections or rejections, the application is submitted as being in condition for allowance which action is earnestly solicited. At a minimum, this Amendment should be entered at least for purposes of Appeal as it either clarifies and/or narrows the issues for consideration by the Board.

If the Examiner has any remaining issues to be addressed, it is believed that prosecution can be expedited and possibly concluded by the Examiner contacting the undersigned attorney for a telephone interview to discuss any such remaining issues.
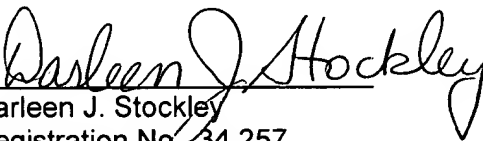
If there are any underpayments or overpayments of fees associated with the filing of this Amendment, please charge and/or credit the same to our Deposit Account No. 19-3935.

Respectfully submitted,

STAAS & HALSEY LLP

Date: February 15, 2007   By: _Darleen J. Hockley_
                               Darleen J. Stockley
                               Registration No. 34,257

1201 New York Avenue, N.W.
Suite 700
Washington, D.C. 20005
Telephone: (202) 434-1500
Facsimile: (202) 434-1501